

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 09:08:03 ; Search time 997.13 Seconds  
(without alignments)  
15746.382 Million cell updates/sec

Title: US-09-001-737-7  
Sequence: 1661  
1 GAATTCGGCTCATATGCA.....TGGCGGATAGCCGGAATTC 1661

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1022815 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	261.8	15.8	878	146	BF275584	BF275584 GA_EB002
2	257.2	15.5	1035	105	AL518632	AL518632 AL518632
3	254	15.3	977	152	BG321293	BG321293 Zm04.0490
4	253.4	15.3	988	106	AL532233	AL532233 AL532233
5	251.6	15.1	955	105	AL515262	AL515262 AL515262
6	249.6	15.0	811	151	BF627437	BF627437 HvME000
7	249.6	15.0	1017	105	AL515579	AL515579 AL515579
8	248	14.9	959	106	AL557150	AL557150 AL557150
9	246.4	14.8	980	106	AL557181	AL557181 AL557181
10	243	14.6	645	113	AM224051	AM224051 EST300862
11	239.4	14.4	716	156	D46006	D46006 R1C510372A
12	237.6	14.3	637	113	AM223768	AM223768 EST300579
13	236.2	14.2	772	151	AM398404	AM398404 EST298251
14	233	14.0	772	151	BF617440	BF617440 HvME000
15	227.4	13.7	680	114	AM330455	AM330455 HvME000
16	227.2	13.7	632	174	BG128308	BG128308 EST473954
17	226	13.6	790	155	BG599254	BG599254 EST504154
18	225.2	13.6	1351	167	BE422296	BE422296 HvME000
19	225.2	13.6	709	21	AL486676	AL486676 EST44998
20	222.2	13.4	825	138	BE642158	BE642158 C12.5.F2
21	222.2	13.4	860	152	BG354884	BG354884 HvME000
22	221.4	13.3	920	106	AL559862	AL559862 AL559862
23	220.8	13.3	920	106	AL559862	AL559862 EST265437
24	220.4	13.3	558	103	AL895994	AL895994 EST473908
25	219	13.2	710	174	BG128262	BG128262 EST473908
26	215.2	13.0	902	106	AL531904	AL531904 AL531904
27	214.4	12.9	817	152	BG344483	BG344483 HvME000
28	214.4	12.9	902	106	AL555787	AL555787 AL555787
29	214.2	12.9	870	152	BG344720	BG344720 HvME000
30	214	12.9	890	105	AL514684	AL514684 AL514684
31	212	12.8	787	155	BG594484	BG594484 EST498162
32	211.2	12.7	671	166	BE318972	BE318972 NF043C12L
33	211	12.7	819	106	AL560505	AL560505 AL560505
34	210.8	12.7	710	163	BE131653	BE131653 L48-1652T
35	209.4	12.6	612	113	AM216817	AM216817 EST29531
36	208.8	12.6	629	149	BF473185	BF473185 HvME000
37	208.8	12.6	715	155	BG592035	BG592035 EST498162
38	208.4	12.5	955	105	AL517839	AL517839 AL517839
39	208.2	12.5	795	174	BG134548	BG134548 EST470110
40	207.4	12.5	739	118	AM622566	AM622566 EST313366
41	204.4	12.3	842	107	AU128717	AU128717 AU128717
42	204.2	12.3	926	106	AL536393	AL536393 AL536393
43	203.6	12.3	855	106	AL557977	AL557977 AL557977
44	202.2	12.2	857	106	AL532194	AL532194 AL532194
45	201.8	12.1	637	155	BG600875	BG600875 EST505770

## ALIGNMENTS

RESULT 1  
LOCUS BF275584 878 bp mRNA EST 07-MAR-2001  
DEFINITION GA\_EB0024G23f Gossypium arboreum 7-10 dpa fiber library Gossypium  
ARBOREUM CDNA clone GA\_EB0024G23f, mRNA sequence.  
ACCESSION BF275584  
VERSION BF275584.1 GI:11206654  
KEYWORDS EST.  
SOURCE Gossypium arboreum.  
ORGANISM Gossypium arboreum.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.  
REFERENCE 1 (bases 1 to 878)  
AUTHORS Wing, R.A., Fritsch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry  
D., Wood, T.C., Leslie, A., and Wilkins, T.A.  
TITLE An integrated analysis of the genetics, development, and evolution

## JOURNAL COMMENT

of the cotton fiber  
Unpublished (2000)  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: TAATACCTCAGTACAGG  
High quality sequence stop: 716.  
Location/Qualifiers  
1. 878  
/organism="Gossypium arboreum"  
/strain="AKA"  
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dpa"  
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## FEATURES

source

BASE COUNT 253 a 157 c 219 g 245 t 4 others  
ORIGIN

Query Match 15.8%; Score 261.8; DB 146; Length 878;  
Best local similarity 58.1%; Pred. No. 1.4e-62;

Matches 458; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

481 TTGAGATATATCTGAGAGATGAGCGGTGGCAACGATGATGATACATCG 540  
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541 AAGATCTCGAGATGAGCGGTGGCAACGATGATGATGATGATGATGATG 600  
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661 CATTTATCTTATGAGAGATGAGCGGTGGCAACGATGATGATGATGATG 720  
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721 AGAAGTCTTAAACCAACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
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328 CTCTGCGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 387  
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901 GTTACAGATTTTACAGAGATGATGATGATGATGATGATGATGATGATGAT 960  
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1081 CTGACTTTGACCTGAAAACTCAAGACCTTTGGCAAAATTAAGTGTGATGCTG 1140  
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Db 628 CTCTGATATTCAGAAAAATTTGGCAGAAAGATTCGCAAACTATCTGCTGTTCAG 687

QY 1141 TTATCAACTAGAGCTCCACAGACAGACCTTTAAAGAAATGAACCTGCATGAG 1200

Db 688 TCATTAAGCTGGGGCTGCACAGACAGACCTTATGAGATGCTAGCTAGCTTGAAG 747

QY 1201 ATGCTTAATGCTACAGCTGACAGCTTGAAGAGTATGCTGCTGCTGCTGGAAC 1260

Db 748 ATGCAAGAAATGCTACATTTGCTGCTCATAGNAGATATGCTGCTGCTGCTGCTG 807

QY 1261 CACTATT 1268

Db 808 CCTAGT 815

RESULT 2

AL518632 1035 bp mRNA EST 13-FEB-2001

LOCUS AL518632 LTI\_NFL011\_NBC1 Homo sapiens cDNA clone CSODN009Y115 5

DEFINITION prime, mRNA sequence.

ACCESSION AL518632

VERSION AL518632.1 GI:12782125

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Source

1..1035

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CSODN009Y115"

/clone\_1lb="LTI\_NFL011\_NBC1"

/sex="male"

/tissue.type="neuroblastoma cells"

/lab\_host="DH10B"

/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 311 a 195 c 259 g 266 t 4 others

ORIGIN

Query Match 15.5% Score 257.2; DB 105; Length 1035;

Best Local Similarity 56.3%; Pred. No. 2,9e-61;

Matches 500; Conservative 1; Mismatches 384; Indels 3; Gaps 1;

QY 18 GCAAAAGAAATCAATTTTCAGAGATGCGCGTGCATGCTGCGGGAGTTGATATG 77

Db 116 GCCAAAGATGTAATTTGGTGCAGATGCCCGAGCTTAATGCTTCAAGAGTGAACCTT 175

QY 78 TTACGATACCGTCAAGTAAAGCTGTGCTCAAGGCGCAATGTTCTTGAAGAA 137

Db 176 TTAGCCGATGCTGCGCGCTTACCAATGGGCCAAGGGAACGATGATTATGAGCAG 235

QY 138 GCTTTGTTCTCCCTTAATTAATGACGGGGTAAACCATGCTTAAGAGATCAATTA 197

Db 236 AGTTGGGGAAGTCCCAAGTAACAAAAGATGTGTGACTGTTCGAAGTCATTCATTA 295

QY 198 GAAGATCATTTTGAAGAAATCATGAGCAAAATGTTGTCTGAGAGGCTTTAAACCAAT 257

Db 296 AAAGATTAATACAAAACATGTGAGCTAACTTTGTAAGATGTTCATTAACACAAAT 355

QY 258 GATATGCTGCTGTGGGAGAGCTACTGACACAGTTTGAACACAGCAATTTGATGA 317

Db 356 GAAGAGCTGGGATGGACCTACACAGCTGCTACTGCTAGCGAGCTCTTAAGCAGGA 415

QY 318 GGACTAAAAAATGTGACAGCAGCTGCTAATCCATTTGGTATCCGTGAGGACATTAACA 377

Db 416 GCTTCGAGAAATAGCAAAAGTCTAATCCAGTGAATCAGAGAGAGGTGATGTTA 475

QY 378 GCAACAGCAACAGCTGTGAGAGCTTGAAGCCATTCCTCAACCTGATTCGCAAGGA 437

Db 476 GCTGTATGCTTATTTCTGATCTCACTTAAAGACAGCTTAACCTGTGACACCCCTTA 535

QY 438 GCTATTGCTGAGTCCCTGCAATATCATCAGCTGCTGAAAAAG--TTGAGAGATATATC 494

Db 536 GAAATTCACAGAGTTCCTGAGATTTCTGCAAAACGAGACAAAGAAATGCGAATATCATC 595

QY 495 TCAGAGCTATGTGAGCGCTGTGGGCAAGATGTGTGATTCATCGAAGAAATCTGAGCT 554

Db 596 TCTGATGCAATGAAAAAGTTGAGAGAGAGGTCTATCAGATTAAGATGAAAAACA 655

QY 555 ATGAAAACAGACTTGAAGCTGTGAGAGCATGCAATTTGACCGTGTACCTGCTCA 614

Db 656 CTGAAGATGATATGAAATTAATTAAGAGCATSCCGTTGATGAGAGCTATATTTCTCA 715

QY 615 TACATGTCACAGACATGAAAAAATGTTGTCAGACCTTGAAGCCATTTATGCTATC 674

Db 716 TACTTATTAATATACATCAAAAGTCCAGAAATGGAATTCAGAGAGCCATGTTCTGTG 775

QY 675 ACGATTAAGAAAGTCCAAACATCCAGACATTTTGCACACTTGTGAGAGATCTTAA 734

Db 776 AGTGAAGAAATTTCTTATGATTCAGCTCATTTGCTGCTGTTGAATGCCAATGCT 835

QY 735 ACCAACCGTCAATCATATTATTCAGATGATGATGATGATGATGATGATGATGATGAT 794

Db 836 CACCGTACCTTTGCTATATGCTGATGATGATGATGATGATGATGATGATGATGATG 895

QY 795 GTCTTGAACATATCGTGTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 854

Db 896 GTCTTGAATAGCTTAAGAGTGTGCTTCAAGTGTGATGATGATGATGATGATGATGATG 955

QY 855 GATGCTGTAAGCTATGCTGAAGACATGCTATCTGACAGTGTG 902

Db 956 TGACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1003

RESULT 3

BG321293

LOCUS BG321293 977 bp mRNA EST 27-FEB-2001

DEFINITION Zm04\_04909\_R Zm04\_AATC\_ECORC\_cold\_stressed\_maize\_seedlings Zea mays

ACCESSION BG321293

VERSION BG321293.1 GI:13150971

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

AUTHORS Singh, J.A., Wakui, K., Couroux, P., De Moors, A., Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Spolt, D. and Finkler, N.A.

TITLE Expressed Sequence Tags from Cold-Stressed Maize Seedlings

JOURNAL Unpublished (2001)

COMMENT Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-Food Canada

960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada



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Db 415 GCCTCGAAGATAGCAAGGTGTAATCCAGTGAATAGAGAGGTGATGTTA 474
Oy 378 GCAAGACAGACAGCTGTGAGCCTTGAAGCCATGCTCAACCTGATCGGACGAA 437
Db 475 GCTGTGATGCTGTATGTTGTAATTAAGACACTGTAACCTGTGACCCCTG 534
Oy 438 GCTATGCTCAGGTGCTGCAATATCATCCAGCTGTAAGAAAG--TTGAGAGTATATC 494
Db 535 GAAATTCACAGGTGCTGATGATTTCTGCAAGGAGACAAAGAAATTCGATATCATC 594
Oy 495 TCAGAGCTATGAGCGTGGGCAAGATGAGGCTATTCATTCGAAAGATCTCAGGT 554
Db 595 TCTGATGCAATGAAAAAGTTGGAGAAAGGGTGTATCAAGTAAGAGTGAAGAAACA 654
Oy 555 ATGGAACAGAACTTGAAGTGTGAAGGATGCAATTTGACCGTGTACTGTCTCAA 614
Db 655 CTGAATGATGATTAAGAAATTAATGAAGCATGAAGTTGATGAGGCTATTTCTGCA 714
Oy 615 TACATGCTCAGACATGAAGAAATGCTTGACACCTTGAAGCCATTTATCTTAATC 674
Db 715 TACTTATTAATACATCAAAAGTCAAGAAATGTGAATTCAGATGCTATGTTCTGTG 774
Oy 675 ACAGATAAAAAGTGTCAAAACATCAAGCAATTTGGCAGTACTTGAAGAGTCTTAA 734
Db 775 AGTGAAGAAAAATTTCTAGTATCCAGTCCATTTGACCTGCTTGAATTTGCCAATGCT 834
Oy 735 ACCAACCTCCATCTACTATTAATGAGATGATGATGATGATGATGATGATGATGATG 794
Db 835 CACCGTAAGCCTTTGGTCAATATCGCTGAAGATGTGATGATGATGATGATGATGATG 894
Oy 795 GCTTGACACAGATTTCTGTACTTCAATGCTGTGCTGCTGAAGCCAGAGATTTGCT 854
Db 895 GCTTGAAATAGGCTAAAGTTGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 954
Oy 855 GATCGTCTGAAGCTATGCTTGAAGACATTTGCTAT 889
Db 955 GACAATAG-AAAGMAGCCTTAAGATATGCTAT 988

RESULT 5
AL515262 955 bp mRNA EST 13-FEB-2001
LOCUS AL515262 L1-NFL006_PL2 Homo sapiens cDNA clone CLOB0162A04 5
DEFINITION AL515262 L1-NFL006_PL2 Homo sapiens cDNA clone CLOB0162A04 5
ACCESSION AL515262
VERSION AL515262.1 GI:12778755
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 955)
AUTHORS L.I.W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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Location/Qualifiers
1..955
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOB0162A04"
/clone_11b="L1-NFL006_PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,"

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BASE COUNT 288 a 181 c 236 g 247 t 3 others
ORIGIN
Query Match 15.1%; Score 251.6; DB 105; Length 955;
Best Local Similarity 57.0%; Pred. No. 1.e-59;
Matches 480; Conservative 0; Mismatches 359; Indels 3; Gaps 1;
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@life.com URL :
http://fulllength.invitrogen.com"
18 GCAAGAAATCAAAATTTTACAGATGCGGCTGCAAGTGGCCGAGTGTATG 77
Db 114 GCAAGATGTAAATTTGGTGCAGATCCGACCTTAATGCTTAAGTGAACCTT 173
Oy 78 TTACAGATACCTTCAAAATGACCTTGTGCTTAAAGGCGCAATGTTGTTGA 137
Db 174 TTACCGATGCTGCGCTTCAATGAGGCGCAAGGAAAGACGTGATTTATGACG 233
Oy 138 GCTTTGTTCTCCCTTAATTAATGACGCGGTAAACATGCTTAAGAGATGCA 197
Db 234 AGTGGGGAGGTCCCAAGTACAAAGATGATGATGATGATGATGATGATGATG 293
Oy 198 GAATGATTTTGAAGATGAGGAGCAAAATGCTGCTGAAGTCTTAAACCAAT 257
Db 294 AAGATTAATTAACAAACATTTGAGACTTAACCTTTCAATGATTTCCATTA 353
Oy 258 GATATTGCTGTGATGAGGACGACTACCAAGTTTGAACAGACATTTGTCANG 317
Db 354 GAGAAAGCTGGGATGCGACTCCACTGCTACTGCTGCTGCTGCTGCTGCTGCT 413
Oy 318 GGAATAAAATGTGACAGGAGGCTGATGATGATGATGATGATGATGATGATG 377
Db 414 GGCTGGAGAGATTAAGCAAGGTGCTATATCAATGATGATGATGATGATGATG 473
Oy 378 GCAAGACAGACAGCTGTGAGACCTTGAAGCCATTTGCTCAACCTGATCTG 437
Db 474 GCTGTGATGCTGATTAATGCTGATTAACCTTAAGAGCTTTAAACCTGTT 533
Oy 438 GCTATTGCTCAGTGTGCTGCAATATCAATCAAGCTCTGAAGAAAG--TTG 494
Db 534 GAAATTCACAGGTGCTACATGATTTCTGCAAGGAGACAAAGAAATTTGCA 593
Oy 495 TCAGAGCTATGAGCGTGTGCGCAAGATGCTGTGATTAACATGAGATCTG 554
Db 594 TCTGATGCAATGAAAAAGTTGGAAGAAAGGCTCATCAGATTAGATGGAACA 653
Oy 555 ATGGAACAGAACTTGAAGTGTGAAGGCAATTTGACCGTGTATCTGCTCAA 614
Db 654 CTGAATGATGATTAAGAAATTAATGAAGGATGAAGTTGATGAGGCTATAT 713
Oy 615 TACATGCTCAGACAGAAATGAAGAAATGCTGACACTTGAAGAACCTTTAT 674
Db 714 TACTTATTAATACATCAAAAGTGCAGAAATGGAATTCACAGATGCTATG 773
Oy 675 ACCGATAAAAGTGTCAAAACATCAAGCAATTTTCCACTACTGAGAGATTTAA 734
Db 774 AGTGAAGAAAAATTTCTAGATATCCAGTCAATGCTGCTGTGAGGTGCCA 833
Oy 735 ACCAACCGCATATCATATGAGATGATGATGATGATGATGATGATGATGATG 794
Db 834 CACCGTAAGCCTTTGGTCAATATGCTGTAAGATGTTGATGAGGCTTAAGT 893
Oy 795 GCTTGACACAGATTTCTGTACTTCAATGCTGTGCTGCTGCTGCTGCTGCT 854
Db 894 GCTTGAATAGCTAAAGTTGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTG 953
Oy 855 GA 856
Db 954 GA 955

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[illegible]

DB	Accession	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
Db	301	ATCCGACCCGGAAGCACTGTATTACAGACAGAGGTTGGACCTCACACTTGACACAAAGCCAGAT	1017 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	948	ATGACAGCCCTTGAGAGGCGCTCTAAAGATTACAGCTGATTAAGATAGACAGCTAATTTGTT	1017 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	361	AACACATGCTTAGAAGACGGCTGTCACAAAGTTGCTCTTACAAAGAAAGTGCACACAACTATGTT	420 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	1008	CAGAGCTTCAGGAAGTTACAGAGCTATTGCTTAACCGTATTATTCACATGATTAATATGCAATTA	1067 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	421	GGTATGCGACGACCCAGAGGAAGTACTAAGAGGGTGGCCACAGATCAAAAAATCTCATT	480 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	1068	GAACAACAACCTCTGACTTTGACCGCGTGAAGAACTCAAGAAACGTTGGCGGAATTAAGCT	1127 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	481	GAGGTACACAGACAGACTAGCAGAGAAAGAAAATCTCAATGAGAGATTTGCAAAAGCTCGCC	540 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	541	GGTGGTGTAGCTGTTATTCAGAGTGGGAGCAACAAAGAACTGAACCTTAAGGGAAGAAAG	600 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	1188	CTTCGCATTGAGGATGCTCTAAATGCTACACAGCGTGAAGCGCTTGGAAGAGTATGCTGCT	1247 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	601	TTGGAGATTGAGAGATGCTCTAAACGACACATAGCTGCGCTTGAGGAAGTATGTGTT	660 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	1248	GGTGGTGAACAACGACCTATTATAGCGTATTGAAAAAGTAGCAGC	1291 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	
Db	661	GGTGGAGCGGTGACCTTTTATGAGCGTGGCTGCTGAAGTTGATGTC	704 bp	AL515579	1	GI:12779072	human.	human sapiens	1017 bp	EST	13-FEB-2001	

FEATURES  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CSDBA002YD20"  
 /clone\_1lb="LTI\_NFL011\_NBC1"  
 /sex="male"  
 /tissue\_type="neuroblastoma cells"  
 /lab\_host="DH10B"  
 /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end clones, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Center Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com url : http://fulllength.invitrogen.com"  
 BASE COUNT  
 308 a 191 c 255 g 261 t 2 others  
 ORIGIN  
 Query Match 15.0%; Score 249.6; DB 105; Length 1017;  
 Best Local Similarity 56.8%; Pred. No. 4e-59;

Matches 478; Conservative 1; Mismatches 360; Indels 3; Gaps 1;

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OY 18 GCAAAAGAAATCAAAATTTTCACAGAGATGCGGTCTCCAGTGGCGGAGATGATATG 77
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Db 116 GCCAAAGATGTAATTTTGTGCGAGATGCCGAGCCCTTAATGCTTCAAGGTGTAGACTT 175
OY 78 TTACGAGATACCGTCACAAAGTAAAGCGTTGTCTTAAAGGCGGAGATGTTGTTGA 137
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Db 176 TTACCGGATGCTGTGCGGCTTACAAATGGGGCCAAAGGAAAGCAAGTATTTATGACAG 235
OY 138 GCTTTGGTTCCTCCCTTAATTAATGAGGGGTAAACCATGCTTAAGAGATGAAATTA 197
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Db 236 AGTTGGGGAAGTCCCAAGTAAACAAAGATGAGTGTGCTGTCGCAAACTCAATGACTTA 295
OY 198 GAGATCATTTTGAACATGAGGAGCAAAATTTGTTCTGAAGTGGCTTCAAAACCAAT 257
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Db 296 AAGATTAATTAACAAAACATGAGGCTAAATCTGTTCAAGATGTTGCCAATTAACAAAT 355
OY 258 GATATGCTGTGTGAGGAGCACTACTGCAAGCTTTTGACAAAGCATTTGTTCAATGA 317
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Db 356 GAAGAGGCTGGGAGTGGGAGTACCACTGCTACTGCTGAGCGCTTATAGCCAAAGAA 415
OY 318 GGAATTAATTAATGACAGAGAGTGTATCCAAATGTTGCTGCGAGGATTTGAACA 377
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Db 416 GGTTCGAGAAAGATTAACAAAGTGTCTAATCCAGTGAATCAGAGAGGTGTGAGTGA 475
OY 378 GCAACAGCAAGAGCTTTGAAGCTTGAAGCCATTGCTCAACTGATCTGCAAGGAA 437
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Db 476 GCTGTGATGCTGTATGTTGCTGAATTAAGCAAGTCAAACTGTGACACCCCTGAA 535
OY 438 GCTATTTGCTGAGTGTGAGTGTGATCATCATGCTCTGAAAAG---TTGAGAGTATATC 494
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Db 536 GAAATTCACAGAGTGTCTGATGATTTCTGCAACGAGGCAAAAGAAATTTGCAATATCATC 595
OY 495 TCAGAGCTATGAGCGGTGTGAGCAACGATGTTGATTCATTCAGATCGAGATCTGAGGT 554
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Db 556 TCTGTGCAATGAAAAAGTGAAGAAAGGTGTGATCACTAAGATTAAGATGAAAAACA 655
OY 555 ATGGAACAGAACTGTGAAGTGTGAGGATGCAATTTTACCTGCTGTTACTGTTCA 614
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Db 656 CTGAATGATGATTAAGAAATTTATGAAGGCAATGAAATTTATGAGGCTATATTTCTTCA 715
OY 615 TACATGCTACACAGCAATGAAAAATGTTGACAGCTTTGAACCCATTTATCTTAATC 674
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Db 716 TACTTTTAAATACATCAAAAGTCAAAATGTGAAATTTCCAGATGCTATGTTCTGTG 775
OY 675 AGGATTAATTAATGTCACAAATCCCAAGACATTTTGGCACTACTGAGGAGTCTTAA 734
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Db 776 AGTAAAGAAATTTCTAGATCCAGTCTGATCTGCTCTTGAATTTGCAATGCT 835
OY 735 ACCAAGCTCATTAATCATTTATGACATGATGATGATGAGCACTTCAACCCCTT 794
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Db 836 CACCGTAAGCTTTGCTGATTAATGCTGAAGATGTTGAGGAGGAGCTTAAGTACACTC 895
OY 795 GTCTTGAACAGATTCGTGTACTTCAATGTTGTTGCTGTCAAGGCGGAGATTTGGT 854
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Db 896 GTCTTGAATAGCTTAAGAGTGTGCTTCAAGTGTGTGCAAGTAAAGCTTCCAGGCTTGGT 955
OY 855 GA 856
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Db 956 GA 957

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Query Match 14.9%; Score 248; DB 106; Length 959;  
Best Local Similarity 56.7%; Pred. No. 1.1e-58;  
Matches 477; Conservative 1; Mismatches 361; Indels 3; Gaps 1;

REFERENCE  
ADPHORS  
TITLE  
JOURNAL  
COMMENT  
Genoscope - Centre National de Sequençage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
1. 959

FEATURES  
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/clone="CS0DH002YB12"  
/clone\_lib="LTI\_FLO12\_Tc1"  
/tissue\_type="T cells from T cell leukemia"  
/note="vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@litech.com URL : http://fulllength.invitrogen.com 1 others

BASE COUNT  
291 a 183 c 238 g 246 t

ORIGIN  
18 GCAAAAGAAATCAAAATTTTCACAGAGATGCGGTCTCCAGTGGCGGAGATGATATG 77  
118 GCCAAAGATGTAATTTTGTGCGAGATGCCGAGCCCTTAATGCTTCAAGGTGTAGACTT 177  
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176 TTACCGGATGCTGTGCGGCTTACAAATGGGGCCAAAGGAAAGCAAGTATTTATGACAG 237  
138 GCTTTGGTTCCTCCCTTAATTAATGAGGGGTAAACCATGCTTAAGAGATGAAATTA 197  
238 AGTTGGGGAAGTCCCAAGTAAACAAAGATGAGTGTGCTGCTGCTTGAATTTGCAATGCT 297  
198 GAGATCATTTTGAACATGAGGAGCAAAATTTGTTCTGAAGTGGCTTCAAAACCAAT 257  
298 AAGATTAATTAACAAAGATTTGAGCTTAACCTGTTCAAGATGTTGCCAATTAACAAAT 357  
258 GATATGCTGTGTGAGGAGCACTACTGCAACAGTTTGAACCAAGCTTGTTCATGAA 317  
358 GAAGAGGCTGGGAGTGGGAGTACCACTGCTACTGATGAGCAACCTCATTAACCAAGAA 417  
318 GGAATTAATTAATGACAGAGTGTATCCAAATGTTGCTGAGGAGCTTAAGAA 377  
418 GGTTCGAGAAAGATTAACAAAGTGTGCTAATCCAGTGAATTAACAGAGAGTGTGATGTA 477  
378 GCAACAGCAAGCTGTGAAGCTTGAAGCCATTGCTCAACCTGATCTGAGCAAGAA 437  
478 GCTGTATGCTGTATTTGCTGAATTAAGAGCTTAAGAGCTTGAACCCCTTGA 537  
438 GCTATGCTGAGTGTGAGTGTGATCATCATGCTCTGAAAAG---TTGAGAGTATATC 494  
538 GAAATTCACAGAGTGTCTGATTAATGCTGAAGGAGCAAAAGAAATTTGCAATATCATC 597  
495 TCAAACTATGAGAGCTGTGGGCAAGATGTTGATTCATTCAGCAAGATTCGAGGT 554  
598 TCTGATGCAATGAAAAAGTTGGAAGAGGTGTCTATCAAGATTAAGATGAAAAACA 657  
555 ATGGAACAGAACTTGAAGTGTGAGGAGTGAATTTACCGTGTACTGTTCTGAA 614





TITLE / Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.  
JOURNAL Unpublished (1999)  
COMMENT Contact: David Frisch  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 4366  
Fax: 864 656 4293  
Email: dfrisch@clemson.edu

FEATURES  
source Location/Qualifiers  
1. 645  
/organism="Lycopersicon esculentum"  
/cultivar="74496"  
/db\_xref="taxon:4081"  
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/clone\_1lb="tomato fruit red ripe, TAMU"  
/tissue-type="pericarp"  
/dev-stage="red ripe (7-20 days post-breaker)"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Supplier: Giovannoni; Fruit were tagged at the  
breaker stage (first sign of lycopene accumulation on the  
blossom end of the fruit) and harvested 7 days  
post-breaker (fully red-ripe). 10 days post breaker, and  
20 days post-breaker (over-ripe). 20 day fruit which  
showed external or internal signs of pathogenesis were  
discarded. Fruit were cut in half and the seeds and  
locules were discarded prior to freezing the pericarp."

BASE COUNT 205 a 102 c 166 g 172 t  
ORIGIN

Query Match 14.6%; Score 243; DB 113; Length 645;  
Best Local Similarity 61.1%; Pred. No. 2,4e-57;  
Matches 393; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

QY 607 TGTCTCATCATGTCACACGATGAAATGATGTCGACACTTGAACCCATTGA 666  
DB 2 TGTCT 111  
QY 667 TCTTATACAGATTAATAAAGTCAACATCAACATTTTGCACACTTGAAGAG 726  
DB 62 TGTCT 121  
QY 727 TTTCTAAACCAACGCTCATCTACTTATGATGATGATGATGATGATGATGAT 786  
DB 122 CTATCAGAAATGTTACCAATTTTATTTTCTGCTGATGATGATGATGATGAT 181  
QY 787 CAACCTTGTCTGACAGATTCGTCTACTTCAATGATGATGATGATGATGATG 846  
DB 182 CAACCTTGTCTGACAGATTCGTCTACTTCAATGATGATGATGATGATGATG 121  
QY 847 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906  
DB 242 GTTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 301  
QY 907 TGTATACAGATCTAGAGCTTAATTAAGATGCTCAATGACACCCCTTGAAG 966  
DB 302 TGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 361  
QY 967 CTGCTAAGATTACAGTTAAGATGACAGATTAATGATGATGATGATGATGAT 1026  
DB 362 CTGCTAAGATTACAGTTAAGATGACAGATTAATGATGATGATGATGATGAT 421  
QY 1027 AAGCTTGTCTAAGCTTGTGACATGATTAATGCAATTAAGAAACAACACTTGA 1086  
DB 422 AAGCTTGTCTAAGCTTGTGACATGATTAATGCAATTAAGAAACAACACTTGA 481  
QY 1087 TTGACCGTGAATAAAGATGATGATGATGATGATGATGATGATGATGATGAT 1146  
DB 482 ATGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 541

QY 1147 AAGTAGAGCTTCAACAGACAGACCTTTAAAGAAATGAATCGCATGAGATGCTC 1206  
DB 542 AAGTAGAGCTTCAACAGACAGACCTTTAAAGAAATGAATCGCATGAGATGCTC 601  
QY 1207 TAAATGCTACAGCTGACGCTTGAAGAGATGATGCTGCTG 1249  
DB 602 TCAATGCAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 644

RESULT 11  
LOCUS D46006 716 bp mRNA EST 09-MAR-2000  
DEFINITION R10S10372A Rice green shoot Oryza sativa cDNA, mRNA sequence.  
ACCESSION D46006  
VERSION D46006.2 GI:7212768  
KEYWORDS EST.  
SOURCE Oryza sativa.  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriaraloideae; Oryzaceae; Oryza.  
1 (bases 1 to 716)  
AUTHORS Sasaki, T., Miyao, A. and Yamamoto, K.  
TITLE Rice cDNA from callus 1995  
JOURNAL Unpublished (1995)  
COMMENT On Mar 9, 1995 this sequence version replaced gi:699715.  
Contact: Takuji Sasaki  
National Institute of Agrobiological Resources  
Rice Genome Research Program  
2-1-2 Kannondai, Tsukuba  
Ibaraki,  
Japan 305  
Tel: 0298-38-7441  
Fax: 0298-38-7468  
Email: tsasakileabr.affrc.go.jp  
PROJECT "RGP"  
Sequence updated (01-Mar-2000).

FEATURES  
source Location/Qualifiers  
1. 716  
/organism="Oryza sativa"  
/strain="Nipponbare"  
/db\_xref="taxon:4530"  
/clone\_1lb="Rice green shoot"  
/note="Green shoot (8 days old)"

BASE COUNT 222 a 120 c 198 g 175 t 1 others  
ORIGIN

Query Match 14.4%; Score 239.4; DB 156; Length 716;  
Best Local Similarity 58.6%; Pred. No. 2,6e-56;  
Matches 414; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 550 GAGGATGGAAGCAAGCTTGAAGTGTGAGGATGATGATGATGATGATGATGAT 609  
DB 5 GAGGATGGAAGCAAGCTTGAAGTGTGAGGATGATGATGATGATGATGATGAT 64  
QY 610 CTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669  
DB 65 CCGGATATTTGTAACGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 124  
QY 670 TATACAGATTAATAAAGTGTCAACATCAACATGATGATGATGATGATGATG 729  
DB 125 TTTTGTGAGCAAAAAAATGACCAAGGAGGATGATGATGATGATGATGATGAT 184  
QY 730 TTAAGCAACCGCTTATCTATGATGATGATGATGATGATGATGATGATGAT 789  
DB 185 TTAAGCAACCGCTTATCTATGATGATGATGATGATGATGATGATGATGAT 244  
QY 790 CCGTGTCTGGAAGATTCGTGATGATGATGATGATGATGATGATGATGATGAT 849  
DB 245 CCGTGTCTGGAAGATTCGTGATGATGATGATGATGATGATGATGATGATGAT 304  
QY 850 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 909

[illegible]

BASE COUNT	204 a	102 c	103 g	168 t	locules were discarded prior to freezing the pericarp.
ORIGIN.					
Query Match	14.3%	Score 237.6;	DB 113;	Length 637;	
Best Local Similarity	60.8%	Pred. No. 8.1e-56;			
Matches 387;	Conservative 0;	Mismatches 249;	Indels 0;	Gaps 0;	
OY	607	TGCTCATACATGTGGTACACAGCAATGAAAAAATGGTTGGAGACCTTGAAACCCCATTTA	666		
DB	2	TCTCTCTCTACTTTTCTTTCACAGAGTGAAAAATGTCCCTTGATATGAGAACTGTAACT	61		
OY	667	TCTTAATCACAGATATAAAAAGTGTCAACATCCAAACATTTTGCCACTACTTGGAGAG	76		
DB	62	TGCTACTGGTTGATATAAAAATATACAAAGCAGAGACTCTTGTAATGTCTGGAAATG	121		
OY	727	TTCTTAAACCAACCGTCCATTCATCTATTTGCAAGATGTATGTGATGGTGAACACTTC	786		
DB	122	CTATCGAATATGGTTTACCCATTTTATATTTGCTGAAATATTTGACAGAGACCTTGG	181		
OY	787	CAACCCCTGTCTGTGAACAATTCGTGGTACTTTCATGTGGTGTGCTGTCAAGAGCGGAC	846		
DB	182	CAACTCTTTTGTCTCAATACATCTTAGAGTGCCCTTGAAGTGCCGTGCATCTTAAGCTCTG	241		
OY	847	GATTGTGATATGTCGTAAAGCTATGCTTGAGACATTCCTATCTTGACAGTGTACAG	906		
DB	242	GTTTGTGTGAGGAAAAAAGCCAGTATCTTGATGACATAGCAACCCCTATCTGAGGCACTG	301		
OY	907	TGATTTCAGAGATCTAGACCTGAAATTTAAAAAGATGCTTAACATAGACAGCCCTTGAAGG	966		
DB	302	TTATTGAGGAGAGAGCTTGGCCCTTACCTTGACAAGGCTGCAGAGAACTTCTAGTCTATG	361		
OY	967	CTGCTTAAGTTATACAGTTGATTAAGATAGACAGATATCTTGAAAGTTGACAGAGTTCAG	1026		
DB	362	CTCTTAAAGTGTGTCTACTTAGAGATGCCACTACACATTTGTTGGTATGTGTAGACTAGG	421		
OY	1027	AAGCTATTGCTACACCGTATTGCACTGATTTAAATGCAATTAGAAMACCAACTTCTGACT	1086		
DB	422	AACCACTCAACAAACGTGTTCACAGATTTTAAAAAAGCTATGAGCGCTGCACATCAATAT	481		
OY	1087	TTGACCGGAAAAAAGCTCAAGAAAGCTTTGGGAAATAGTGGTGGTGTACCTTTTCTCA	1146		
DB	482	ATGAAAAAGAAAGAACTTAATGAAAGAAATTTGCTAAGTTATACAGAGGTGTGGCTGTAC	541		
OY	1147	AAGTAGAGCTTCCAAACAGAGACAGCTTTTAAAAAGAAATGAACCTTGCAATGAGAGCTTC	1206		
DB	542	AGGTGTGAGCTCAACATCGAAATGAAATGAAAGAAAGAAACCTTAGATAGAAATGCTTC	601		
OY	1207	TAAATGCTACACGTGCAGCCGTTGAGAAGAGATATCG	1242		
DB	602	TCAATGCCAACAAAGCAGCTGTTGAGAAAGTATG	637		
LOCUS	AM398404				
LOCUS	AM398404	668 bp	mRNA	EST	07-FEB-2000
DEFINITION	EST296251 L. pennellii trichome, Cornell University Lycopersicon				
	pennellii cDNA clone cLPT6M1 5' similar to similar to nearly				
	identical to Solanum tuberosum chaperonin-60 beta subunit, mRNA				
	sequence.				
ACCESSION	AM398404				
VERSION	AM398404				
KEYWORDS	AM398404.1 GI:6916874				
SOURCE	EST.				
ORGANISM	Lycopersicon pennellii.				
	Lycopersicon pennellii.				
	Eubryot, Vitidiplante, Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots;				
	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;				
	Lycopersicon.				
	1 (bases 1 to 668)				
REFERENCE	Alcala, J., Vrebalov, J., White, R., Matern, A. L., Lakey, J., Holt, I. E.,				
AUTHORS	Liang, F., Hansen, T. S., Upton, J., Bonning, C. M., Craven, M. B., Fujii				

TITLE  
'C.V., Bowman, C.L., Nierman, M., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.  
Generation of ESTs from wild tomato (*Lycopersicon pennellii*)  
trichomes  
Unpublished (1999)  
JOURNAL  
Contact: David Fritsch  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 4366  
Fax: 864 656 4293  
Email: dfritsch@clemson.edu  
COMMENT  
5 prime sequence.

## FEATURES

source  
Location/Qualifiers

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/organism="Lycopersicon pennellii"  
/db\_xref="taxon:28526"  
/clone\_lib="L. pennellii trichome, Cornell University"  
/tissue\_type="trichome"  
/dev\_stage="mixed stages"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."  
BASE COUNT 209 a 104 c 177 g 178 t  
ORIGIN

Query Match 14.2% Score 236.2; DB 115; Length 668;  
Best Local Similarity 59.7% Pred. No. 2e-55;

Matches 397; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

QY 513 GTGGGCAACGATGGTGTGATTCATCGAAGATCTCAGGTATGGAACAGACAGATTGAA 572  
DB 4 GTTGGAGAGAGAGGTGTGTGACACAGAGAGGTAAAGTCTGAAACAGCTGCGCT 63  
QY 573 GTGGTGAAGCATGCAATTTGACCGTGTACCGTCAATACATGCTGACAGACAT 632  
DB 64 GTGGTGAAGCATGCAATTTGACCGTGTACCGTCAATACATGCTGACAGACAT 123  
QY 633 GAAAAATGCTGCAGACCTTGAAAAACCAATTAATCTTAATCAAGGATAAAGTCTCA 692  
DB 124 GAGAAAAATGCTGCAGACCTTGAAAAACCAATTAATCTTAATCAAGGATAAAGTCTCA 183  
QY 693 AACATCCAGACATTTGGCAGTCTGAGAGATTTCTTAACCAACCGTCCATTAATC 752  
DB 184 AATGCAAGAGATCTTGTATATGCTTGAAGATCTTCAAGAAATGTTACCAATTTTA 243  
QY 753 AATATGCAAGATCTTGTATATGCTTGAAGATCTTCAAGAAATGTTACCAATTTTA 812  
DB 244 AATATGCTTAAGATTAATGAGAGACCTTTGCAACCTTTGTCATTAATGAGTGA 303  
QY 813 GTTACTTCAATGCTGCTCTCAAGCGCCAGAGATTTGATGATGCTGTAAGCTATG 872  
DB 304 GGTGCTTGAAGGTCCCTCACTTAAGCTCTGCTGTTGAGAGAAAAAGCAGAT 363  
QY 873 CTTAAGACATGCTCTTGTGACAGGTGCTGATTAATCAAGAGATCTGAGACTGAA 932  
DB 364 CTTAATGACATGACCACTTGTGAGAGCTGTTATTAAGAGAGCTGGCCCTTACC 423  
QY 933 TTAAGAGATCTCAATGACAGCCCTTGAGAGGCTGCTCAAGATTAATCAAGTGAAT 992  
DB 424 TTGAGACAGGCTGACAGAGAGTTCTAGGTCAATGCTGAAGTGTGCTGATCAAT 483  
QY 993 AGCAGATTAATTTGAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCA 1052  
DB 484 GCCATCAATTTGTTGAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCA 543  
QY 1053 ATTAATGCAATTAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCA 1112  
DB 1112 ATTAATGCAATTAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCA

DB 544 ATTAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCA 603  
QY 1113 TTGCGCAATTAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCA 1172  
DB 604 ATTTCAATTAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCA 663  
QY 1173 TTAA 1177  
DB 664 TTGA 668

## RESULT 14

LOCUS BF617440 772 bp mRNA EST 22-FEB-2001  
DEFINITION HVSMC0017F22F Hordeum vulgare seedling shoot EST library  
HYDRA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone  
HVSMC0017F22F, mRNA sequence.  
ACCESSION BF617440.2 GI:1108972  
VERSION  
KEYWORDS EST.

## SOURCE

ORGANISM  
barley.

Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
; Triticeae; Hordeum.  
1 (bases 1 to 772)  
Wing, R., Close, T.J., Kleinholz, A., Wise, R., Begum, D., Fritsch, D., Yu  
T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and  
Wood, T.

## REFERENCE

AUTHORS

TITLE  
Development of a genetically and physically anchored EST resource  
for barley genomics  
Unpublished (2000)  
On Dec 18, 2000 this sequence version replaced gi:11881174.  
CONTACT: Wing RA  
Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: AATTAACCTCACTTAAGAGG  
High quality sequence stop: 719.  
Location/Qualifiers

## FEATURES

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/tissue\_type="Seedling shoot"  
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ORIGIN

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Best Local Similarity 57.9% Pred. No. 1.7e-54;

Matches 413; Conservative 0; Mismatches 300; Indels 0; Gaps 0;

QY 478 AAGTTGAGAGATTAATCTCAAGAGCTATGAGAGCTGTGGCAGACATGCTGTGATTACCA 537  
DB 37 AATGCGTATACATGATATGACAGAGCTTATGCAAGTTGCGGAGAGAGTGTATACC 96  
QY 538 TCGAAGATCTCGAGGATATGGAAGCAAGACTGAAGTGTGAAGCATGCAATTTGACC 597  
DB 97 TTGAAGAGGAGGAGATTCGAGAACAACTTTATGTTGTGGAGGAATCGAGTTGAGC 156  
QY 598 GTGGTACCTGCTCAATACATGATGTCACAGCAAGAAATGAGTTGGACAGACTTGAAA 657  
DB 157 GTGGTATATCTATCTTATTTGTTACGACAGAGAGAAATGACCAACGAGTACGAGA 216

QY	658	ACCATTTATCTTAACAGCGATATAAAAAGTCCAAACATCCAAACATTTTGGCACTAC	717
Db	217	ACTGCAGAGCTGCTTTGGTTTGACAGAAATACACCAACGCGGGATCTTTATCATAGTTTC	276
QY	718	TTGAGGAGTTCTTAAAMCAACCGCTCCATTACTCATTTATTCAGATGATGTGATGGTG	777
Db	277	TGGAGGAGGACCATTTAGGGGTCAATACCACATCTCGATTCATTTCTGAGATATGAGCAGG	336
QY	778	AAGCACTTCCAAACCTTGCTCTTGAACAAGATGTGTGTACTTCAATGTGGTGTGCTCA	837
Db	-337	AGGCTCTGCAACCCCTGTGTGTGTCACCAACGATTAAGAGTCTTTGAAATCTGTCTATTC	396
QY	838	AAGCCCGAGATTTGGTGTATGCTGTGAAGCTATGCTTTGAAGACATTCATTTCTTGACAG	897
Db	397	AAGCCCTGCTTTTGGAGAGGCAAGACCCAGTACCTGGACACATTCCTCATCCACCG	456
QY	898	GTGTACAGATTTACAGAGATCTAGAGACTTAATTAAMAGATCTACATGACACGCC	957
Db	457	GAGGAATGTTATCAGAGACGAGGTGTGACTCATCTTACAAAGCAGATATACAGAGTTG	516
QY	958	TTGACACAGCTGTGAAGATTCAGTTGATTAATATGACACAGTATTTGTTGAGAGTTCA	1017
Db	517	TAGGAAGGCTGTGAAGGTGTGCTCTTCAAAAGAGTGCAGCAACAATTAAGTTGGATGGCA	576
QY	1018	GAACTTCAGAGCTATTTCTACACGCTATTGCTAGTGTAAATCGCAATTAAGAAACAACAA	1077
Db	577	GCACCCCGAGGAAGATGACTATGAGAGGGTTGCACAGATTCAAAATCTATTTGAGGTGACAG	636
QY	1078	CTTGTGACTTTGACGGTAAATAACTACAAACGTTTGGCCGAATTAAGTGTGTGTATG	1137
Db	637	AGCAAGACTACGAGAGAAACCTCATATGAAGATTCGCAAAAGTCTCCCGGTGGGTG	696
QY	1138	CTGTATCAAGTAGAGCTCCAAACAGACAGACGCTTTAAAGCAATGAACCTT	1190
Db	697	CTGTATTCAGGTGGAGCACAAACAGAACTGACTTAAGAGAGAAAGTT	749
RESULT 15			
AM310455			
LOCUS			
DEFINITION	AM310455 680 bp mRNA	EST	31-JAN-2000
ACCESSION	PF0VAFCB331SK Onchocerca volutus adult female cDNA following		
VERSION	1.1		
KEYWORDS	ivermectin [SAM98PF-OVAF] Onchocerca volutus cDNA clone		
SOURCE	AM310455.1 GI:6826808		
ORGANISM	Onchocerca volutus.		
	Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae.		
REFERENCE	Onchocercidae: Onchocerca.		
AUTHORS	1 (bases 1 to 680)		
TITLE	Fischer, P. and Williams, S.A.		
JOURNAL	Genes Expressed in adult female stage of Onchocerca volutus		
COMMENT	following treatment with ivermectin		
	Unpublished (1999)		
	Contact: Peter Fischer		
	Molecular Parasitology		
	Bernhard Nocht Institute for Tropical Medicine		
	Bernhard-Nocht-Strasse 74, 20359 Hamburg, Germany		
	Tel: 49 40 42818 486		
	Fax: 49 40 42818 400		
	Email: pfischer@bni.uni-hamburg.de		
	Seq primer: pBluescript SK.		
	Location/Qualifiers		
	1..680		
FEATURES			
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	/db_xref="taxon:6282"		
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	/sex="female"		
	/dev_stage="adult"		

BASE COUNT  
ORIGIN

230 a 53 c 151 g 204 t 2 others

/lab-host="X1:Blue MRP"  
/note="Vector: Lambda Uni-ZAP XR; Site: 1: Eco RI; Site: 2:  
Xho I; Filarial nematode parasite of humans. Two adult  
female worms of *Onchocerca volvulus* were isolated from  
one consenting patient from western Uganda. The patient  
was treated 28 hours and 7 month before nodulectomy with  
single dose of 150 mg/Kg ivermectin. Adult female worms  
were quick frozen. Their mRNA was converted to  
double-stranded cDNA using reverse transcriptase and  
oligo(dT) followed by RNase H and DNA pol. I. The library  
has 2.9 x 10E5 independent recombinants and the average  
insert size is ~800bp. The library was constructed by  
Peter Fischer with worms provided by Dr. Dietrich W.  
Buttner. The library is available from Dr. Steven A.  
Williams (U.S.A.) or Dr. Peter Fischer (Germany), email:  
genome@smith.edu, fischp@ecol.com"

```

Query Match: 13.7%; Score 227.4; DB 114; Length 680;
Best Local Similarity 61.2%; Pred. No. 6, 2e-53;
Matches 385; Conservative 0; Mismatches 241; Indels 3; Gaps 1

Qy 611 TCATATCATGTGCACAGCAATATAAAAATGGTTGCAGACCTTGGAAAACCCATTATCTT 670
Db 1 TCCGATATTTTATATCAATATATGAGAAAATGATGTGAGAGTGAAGATCCCATATCTTT 60
Qy 671 AATCAGGATATAAAAAGTGTCAACATCCACAGACATTTTGGCCACTACTGAGAGATCTT 730
Db 61 AATTACAGAAAAAACTTAATATTTACGCTTTGCTTTATCTTCTTGAAGCTGTCT 120
Qy 731 TAAACCAACCGTCCATTACTCTATTATTCAGATGATGTGATGTGGAAGCACTTCCAC 790
Db 121 TAAGTCTGTAAACCTTTACTCTATCTATTCAGAAAGACATTTGAGGGTGAAGCAATTAAATAC 180
Qy 791 CCTGTCTTGAACAGATTCGTGGTACTTTCATATGTGGTTGCTGTCAAAAGCCCAAGAT 850
Db 181 TTATGATTTATTAATTAAGTTGGCTGAGAGCTTAAGATTTGCTGACAGTCAAGCTT 240
Qy 851 TGGTATGCTGTAAACCTATGCTTGAAGACATTTGCTATCTGTGACAGGTGTA---CAGT 907
Db 241 TGGTATGTAAGAAAGAGAGATGCTTGAAGATATATGACAGCTTTAACTTAATGCTTAAGTATGT 300
Qy 908 GATTACAGAGGANTCTAGACCTTGAATTAAGAATGCTACATAGACAGCCCTTGGACAGGC 967
Db 301 CATAAAAAGATTAACCTTGGGATTTAAATGGAAGACCTTAACCTTGAAGACCTTGGCATATGC 360
Qy 968 TGGTAAAGTTTACCTTATTAAGATATAGCAAGTAAATTTGGAGGTTCAGSAGTGTGA 1027
Db 361 TAAAAATTTAAATCTATTAAGATATATATCTACATTTGTTAGCGAAATATAGTCTACTGA 420
Qy 1028 AGCTATTCCTAACCGTATTCGACTGATTAATTCGAAATAGAAACAACACTTCTGACTT 1087
Db 421 CAGAGTAAACCTTGAATTTGAGAGATTTAAATCTCAATATGAGCTTCAACTTCGTATTA 480
Qy 1088 TGACCGTGAATAAATCTAACAAGACGTTGGCCGAATTTAGCTGTGGTATGCTATATCA 1147
Db 481 TGATTAAGAGAAATTAAGAGAGCGTTTACGAAATTTATCAGAGTGGTGTCTGCTACTAA 540
Qy 1148 AGTAGAGACTTCAACAGAGACAGCTTTTAAAGAAATAAATCTTCGATTTGAGATGCTCT 1207
Db 541 AATTGGTGTGAGACACTGTAATTTAGAAATTTAAAGAAAGTAAAGATATGGGTGAGAGATGCTT 600
Qy 1208 AATATGCTACAGCTTCAGCGTGTGAAGAAG 1236
Db 601 GCAGCCACACAGAGCTGCAATTAGAGSAG 629

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Job time: 3752 sec

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